

SEQUENCE LISTING

<110> Wu, Guang-Jer

<120> Diagnostic for Metastatic Prostate Cancer

<130> 95-97

<140> US unassigned

<141> 2000-09-01

<150> US 60/076,664

<151> 1998-03-03

<150> PCT US99/04850

<151> 1999-03-02

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 1950

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1938)

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Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

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cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg aag tgc 144

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

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ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg ttt tct 192

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Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

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ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc cag gac	288
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp	
85 90 95	
aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac gag cgc	336
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg	
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atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac cgc atc	384
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile	
115 120 125	
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Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn	
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Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr	
145 150 155 160	
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Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys	
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Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser	
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Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu	
195 200 205	
aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac tgt gag	672
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu	
210 215 220	
ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc agg gaa	720
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu	
225 230 235 240	
gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg gaa gtg	768
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val	
245 250 255	
gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc agg tgt	816
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys	
260 265 270	
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Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn	
275 280 285	

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Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val	
290 295 300	
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Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys	
305 310 315 320	
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Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln	
325 330 335	
gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc gca gcc	1056
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala	
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cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag gca gag	1104
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu	
355 360 365	
agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca ggc cag	1152
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln	
370 375 380	
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Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly	
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Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp	
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Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu	
435 440 445	
aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc tcc tgg	1392
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp	
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aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag cga gtc	1440
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val	
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Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly	
485 490 495	

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Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
500 505 510

ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc aac aca 1584
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
515 520 525

acc act ggc ctc agc act tcc act gcc agt cct cat acc aga gcc aac 1632
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
530 535 540

agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg ggc gtg 1680
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
545 550 555 560

gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg ctg ggc 1728
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
565 570 575

gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc agg cgc 1776
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
580 585 590

tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag agc gaa ctt 1824
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu
595 600 605

gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc ctc ctg 1872
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
610 615 620

cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga gag aaa 1920
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<211> 646

<212> PRT

<213> Homo sapiens

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Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
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Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
 50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
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 85 90 95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
 100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
 115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
 130 135 140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
 145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
 165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
 180 185 190

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
 195 200 205

Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
 210 215 220

Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
 225 230 235 240

Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
 245 250 255

Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
 260 265 270

Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
 275 280 285

Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
 290 295 300

Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys																			
305					310				315										320
Gln Gly Leu Asp Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln					325				330										335
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala					340				345										350
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu					355				360										365
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Gly Gln					370				375										380
Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu					385				390										400
Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly					405				410										415
Leu Asn Arg Thr Gln Leu Val Asn Val Ala Ile Phe Gly Pro Pro Trp					420				425										430
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu					435				440										445
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp					450				455										460
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val					465				470										475
																			480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly					485				490										495
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu					500				505										510
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr					515				520										525
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn					530				535										540
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val					545				550										555
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Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly					565				570										575

Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
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Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Ser Glu Leu
595 600 605

Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
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Tyr Ile Asp Leu Arg His
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<213> Homo sapiens

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<222> (8)..(1945)

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Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln
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cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg 145
Pro Ala Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu
35 40 45

aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg 193
Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp
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ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag 241
Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln
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ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc 289
Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu
80 85 90

cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac	337
Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp	
95 100 105 110	
gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac	385
Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr	
115 120 125	
cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag	433
Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln	
130 135 140	
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Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val	
145 150 155	
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Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp	
160 165 170	
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Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile	
175 180 185 190	
cag tcg tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt	625
Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser	
195 200 205	
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Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr	
210 215 220	
tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc	721
Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser	
225 230 235	
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Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu	
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Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile	
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Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn	
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305 310 315	
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Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu	
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Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro	
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Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr	
370 375 380	
gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa	1201
Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys	
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Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile	
400 405 410	
ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc	1297
Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro	
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Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln	
465 470 475	
cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag	1489
Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu	
480 485 490	
aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc	1537
Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser	
495 500 505 510	

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Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser	
515 520 525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga	1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg	
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gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg	1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg	
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ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg	1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val	
560 565 570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc	1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys	
575 580 585 590	
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Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr	
595 600 605	
gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc	1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly	
610 615 620	
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga	1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly	
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 35 40 45

Gly	Leu	Ser	Gln	Ser	Gln	Gly	Asn	Leu	Ser	His	Val	Asp	Trp	Phe	Ser	50	55	60	
Val	His	Lys	Glu	Lys	Arg	Thr	Leu	Ile	Phe	Arg	Val	Arg	Gln	Gly	Gln	65	70	75	80
Gly	Gln	Ser	Glu	Pro	Gly	Glu	Tyr	Glu	Gln	Arg	Leu	Ser	Leu	Gln	Asp	85	90	95	
Arg	Gly	Ala	Thr	Leu	Ala	Leu	Thr	Gln	Val	Thr	Pro	Gln	Asp	Glu	Arg	100	105	110	
Ile	Phe	Leu	Cys	Gln	Gly	Lys	Arg	Pro	Arg	Ser	Gln	Glu	Tyr	Arg	Ile	115	120	125	
Gln	Leu	Arg	Val	Tyr	Lys	Ala	Pro	Glu	Glu	Pro	Asn	Ile	Gln	Val	Asn	130	135	140	
Pro	Leu	Gly	Ile	Pro	Val	Asn	Ser	Lys	Glu	Pro	Glu	Glu	Val	Ala	Thr	145	150	155	160
Cys	Val	Gly	Arg	Asn	Gly	Tyr	Pro	Ile	Pro	Gln	Val	Ile	Trp	Tyr	Lys	165	170	175	
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Ser	Gln	Thr	Val	Glu	Ser	Ser	Gly	Leu	Tyr	Thr	Leu	Gln	Ser	Ile	Leu	195	200	205	
Lys	Ala	Gln	Leu	Val	Lys	Glu	Asp	Lys	Asp	Ala	Gln	Phe	Tyr	Cys	Glu	210	215	220	
Leu	Asn	Tyr	Arg	Leu	Pro	Ser	Gly	Asn	His	Met	Lys	Glu	Ser	Arg	Glu	225	230	235	240
Val	Thr	Val	Pro	Val	Phe	Tyr	Pro	Thr	Glu	Lys	Val	Trp	Leu	Glu	Val	245	250	255	
Glu	Pro	Val	Gly	Met	Leu	Lys	Glu	Gly	Asp	Arg	Val	Glu	Ile	Arg	Cys	260	265	270	
Leu	Ala	Asp	Gly	Asn	Pro	Pro	Pro	His	Phe	Ser	Ile	Ser	Lys	Gln	Asn	275	280	285	
Pro	Ser	Thr	Arg	Glu	Ala	Glu	Glu	Glu	Thr	Thr	Asn	Asp	Asn	Gly	Val	290	295	300	
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 325 330 335

Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
 340 345 350

Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
 355 360 365

Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
 370 375 380

Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
 385 390 395 400

Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly
 405 410 415

Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp
 420 425 430

Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
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Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
 450 455 460

Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
 465 470 475 480

Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
 485 490 495

Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
 500 505 510

Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
 515 520 525

Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
 530 535 540

Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
 545 550 555 560

Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
 565 570 575

Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
 580 585 590

Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu
595 600 605

Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
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Tyr Ile Asp Leu Arg His
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<210> 5
<211> 1962
<212> DNA
<213> Artificial Sequence

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cDNA, AS MODIFIED TO FACILITATE CLONING

<400> 5
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<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence: OLIGONUCLEOTIDE, FOR SUBCLONING HUMAN
 MUC18 FRAGMENT

<400> 6
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<210> 7

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:OLIGONUCLEOTIDE, FOR SUBCLONING HUMAN
MUC18

<400> 7
ctggaactcg aggtcctggc tactctc

27

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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SEQUENCE ENCODED BY PORTION OF PGEX-6P-1 VECTOR

<400> 8
Gly Pro Leu Gly Ser
1 5

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:OLIGONUCLEOTIDE, SEQUENCE CORRESPONDS TO
HUMAN MUC18

<400> 9
ctcgggatcc atggggcttc ccaggct

27

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:OLIGONUCLEOTIDE, SEQUENCE CORRESPONDS TO
HUMAN MUC18

<400> 10

tcggggctaa tgcctcagat cgatg

25

<210> 11

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: JUNCTION
SEQUENCE FOR MCU18 CLONED INSERT

<400> 11

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ccgcacgtg actgactgac g

81

<210> 12

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: JUNCTION
SEQUENCE FOR CLONED MUC18 INSERT

<400> 12

Leu Glu Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Glu Phe Pro Gly

1

5

10

15

Arg Leu Glu Arg Pro His Arg Asp

20

<210> 13

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: JUNCTION
SEQUENCE FOR CLONED MUC18 INSERT

<400> 13

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81

<210> 14

<211> 23

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:JUNCTION
SEQUENCE IN FUSION PROTEIN

<400> 14
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1 5 10 15

Ser Thr Arg Ala Ala Ala Ser
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<210> 15
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:JUNCTION
SEQUENCE IN VECTOR WITH MCU18 CLONED INSERT

<400> 15
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cgcatcgtga ctgactga 78

<210> 16
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:JUNCTION OF
FUSION PEPTIDE

<400> 16
Leu Gly Val Leu Phe Gln Gly Pro Leu Gly Ser Pro Asn Ser Arg Val
1 5 10 15

Asp Ser Ser Gly Arg Ile Val Thr Asp
20 25